

Amendments to the Claims

1. (Currently amended) A method of separating a population of duplexes, each comprising one of a population of different, substantially uncharged oligomeric analyte molecules and hybridized with a specific probe molecule,

wherein said substantially uncharged analyte molecules are oligonucleotide analogs composed of linked subunits of which at least 90% are uncharged, and said specific probe molecule is a fully charged nucleic acid or fully charged nucleic acid analog,

the method comprising:

(a) applying to a charge-bearing separation medium a mixture of (i) the different substantially uncharged analyte molecules and (ii) the specific probe molecule, under conditions such that the probe forms stable duplexes with a plurality of or all of the different analyte molecules,

thereby forming a plurality of different probe-analyte duplexes, which differ from each other with respect to the presence, length or position of an unhybridized portion of the probe molecule,

~~a mixture of species selected from probe-analyte duplexes, single stranded analyte, single stranded probe, and combinations thereof; and~~

(b) separating said different probe-analyte duplexes from each other and from single stranded analyte or probe molecules species within the medium.

2. (Currently amended) The method of claim 1, wherein ~~the nucleotide sequence of each~~ analyte molecule has a nucleotide sequence is selected from the group consisting of a selected sequence, different length fragments of the selected sequence, internal deletion or insertion variants of the selected sequence, mutation variants of the selected sequence, and combinations thereof.

3. (Original) The method of claim 2, wherein said deletion, insertion or mutation variants contain at most one such deletion, insertion or mutation per 8 nucleotides of the selected sequence.

4. (Cancelled)
5. (Original) The method of claim 2, wherein the probe includes a sequence complementary to the selected sequence.
6. (Previously presented) The method of claim 5, wherein the probe has a length which is equal to, or up to 25% greater than, the length of the selected sequence.
7. (Currently amended) The method of claim 2, wherein the probe includes a sequence complementary to an N-1 deletion variant of the selected sequence, N being the length in nucleotides of the selected sequence.
8. (Original) The method of claim 7, wherein the probe has a length equal to said N-1 deletion variant of the selected sequence.
9. (Original) The method of claim 8, wherein said conditions are such that said probe hybridizes to only said N-1 deletion variant.
10. (Original) The method of claim 2, wherein variations in sequence or length among said analyte molecules occur within a given subregion of said selected sequence, and the probe is effective to stably hybridize to said subregion under the conditions of said analysis.
11. (Original) The method of claim 10, wherein the population contains analyte molecules which are N-1 deletion variants of the selected sequence, and the probe has a sequence and length sufficient to stably hybridize to each analyte molecule, under the conditions of said separating, at a region of the analyte molecule containing a deletion site.
- 12-14. (Cancelled)
15. (Original) The method of claim 1, wherein the charge bearing support is an ion exchange medium, and said separating of step (b) comprises passing an eluant through the medium.

16. (Previously presented) The method of claim 1, wherein the charge bearing separation medium is an electrophoresis medium, and said separating of step (b) comprises applying an electric field between opposing boundaries of the medium.

17. (Original) The method of claim 16, wherein the medium includes a superimposed pH gradient.

18. (Cancelled)

19. (Previously presented) The method of claim 1, wherein all of said subunits are uncharged.

20. (Currently amended) The method of claim 1, wherein the analyte molecules are selected from the group consisting of peptide nucleic acids, phosphotriester oligonucleotides, methylphosphonate oligonucleotides, morpholino oligomers, and chimeras of any member of this group with another member of this group or with DNA, 2'-O-alkyl RNA, or 2'-O-allyl RNA.

21. (Original) The method of claim 20, wherein the analyte molecules are morpholino oligomers.

22. (Original) The method of claim 21, wherein said morpholino oligomers have intersubunit linkages selected from the group consisting of phosphoramidate and phosphorodiamidate.

23. (Original) The method of claim 1, wherein the probe is selected from the group consisting of DNA, RNA, 2'-O-alkyl RNA, 2'-O-allyl RNA, phosphorothioate DNA, and chimeras thereof.

24. (Original) The method of claim 23, wherein the nucleic acid is DNA.

25. (Original) The method of claim 1, wherein the probe is labeled.

26. (Original) The method of claim 25, further comprising the step of detecting and quantitating a duplex of the labeled probe with at least one target analyte molecule in the population.

27. (Original) The method of claim 1, further comprising the step of isolating at least one said duplex.